

Figure 42

Figure 42: An alignment of the IFN-gamma nucleotide sequences from human, cat, rodent species.

AF081502 Marmota monax IFN-gamma	(1)	1	50
D30619 Felis catus IFN-gamma	(1)	CTACTGATTTCAACTTCTTTTCCCTTACGATTT--CGATTCATGATTTAC	
X87308 Homo sapien IFN-gamma	(1)	-----	
AF081502 Marmota monax IFN-gamma	(31)	51	100
D30619 Felis catus IFN-gamma	(49)	ACAGCTGATTTCCTGCTTTTCTAGGCTCGGATCATTTCGCTTCCTAG	
X87308 Homo sapien IFN-gamma	(1)	ACAGCTGATTTCCTGCTTTTCTAGGCTCGGATCATTTCGCTTCCTAG	
AF081502 Marmota monax IFN-gamma	(81)	101	150
D30619 Felis catus IFN-gamma	(99)	CTGTTAGCCGACGGCTCGCTAAATATGATATAGTTTAAATAGAT	
X87308 Homo sapien IFN-gamma	(1)	CTGTTAGCCGACGGCTCGCTAAATATGATATAGTTTAAATAGAT	
AF081502 Marmota monax IFN-gamma	(131)	151	200
D30619 Felis catus IFN-gamma	(149)	ATTATATGCTGAGGCTATGTTTAAATATGATATAGTTTAAATAGAT	
X87308 Homo sapien IFN-gamma	(50)	ATTATATGCTGAGGCTATGTTTAAATATGATATAGTTTAAATAGAT	
AF081502 Marmota monax IFN-gamma	(181)	201	250
D30619 Felis catus IFN-gamma	(199)	GTTATATGCTGAGGCTATGTTTAAATATGATATAGTTTAAATAGAT	
X87308 Homo sapien IFN-gamma	(100)	GTTATATGCTGAGGCTATGTTTAAATATGATATAGTTTAAATAGAT	
AF081502 Marmota monax IFN-gamma	(231)	251	300
D30619 Felis catus IFN-gamma	(249)	CGATATGCTGAGGCTATGTTTAAATATGATATAGTTTAAATAGAT	
X87308 Homo sapien IFN-gamma	(150)	CGATATGCTGAGGCTATGTTTAAATATGATATAGTTTAAATAGAT	
AF081502 Marmota monax IFN-gamma	(279)	301	350
D30619 Felis catus IFN-gamma	(299)	CGATATGCTGAGGCTATGTTTAAATATGATATAGTTTAAATAGAT	
X87308 Homo sapien IFN-gamma	(198)	CGATATGCTGAGGCTATGTTTAAATATGATATAGTTTAAATAGAT	
AF081502 Marmota monax IFN-gamma	(328)	351	400
D30619 Felis catus IFN-gamma	(349)	CGATATGCTGAGGCTATGTTTAAATATGATATAGTTTAAATAGAT	
X87308 Homo sapien IFN-gamma	(247)	CGATATGCTGAGGCTATGTTTAAATATGATATAGTTTAAATAGAT	
AF081502 Marmota monax IFN-gamma	(378)	401	450
D30619 Felis catus IFN-gamma	(399)	CGATATGCTGAGGCTATGTTTAAATATGATATAGTTTAAATAGAT	
X87308 Homo sapien IFN-gamma	(297)	CGATATGCTGAGGCTATGTTTAAATATGATATAGTTTAAATAGAT	
AF081502 Marmota monax IFN-gamma	(428)	451	500
D30619 Felis catus IFN-gamma	(449)	CGATATGCTGAGGCTATGTTTAAATATGATATAGTTTAAATAGAT	
X87308 Homo sapien IFN-gamma	(347)	CGATATGCTGAGGCTATGTTTAAATATGATATAGTTTAAATAGAT	
AF081502 Marmota monax IFN-gamma	(478)	501	550
D30619 Felis catus IFN-gamma	(499)	CGATATGCTGAGGCTATGTTTAAATATGATATAGTTTAAATAGAT	
X87308 Homo sapien IFN-gamma	(397)	CGATATGCTGAGGCTATGTTTAAATATGATATAGTTTAAATAGAT	
AF081502 Marmota monax IFN-gamma	(528)	551	569
D30619 Felis catus IFN-gamma	(549)	CGATATGCTGAGGCTATGTTTAAATATGATATAGTTTAAATAGAT	
X87308 Homo sapien IFN-gamma	(439)	CGATATGCTGAGGCTATGTTTAAATATGATATAGTTTAAATAGAT	

GigaMatrix™ Applications

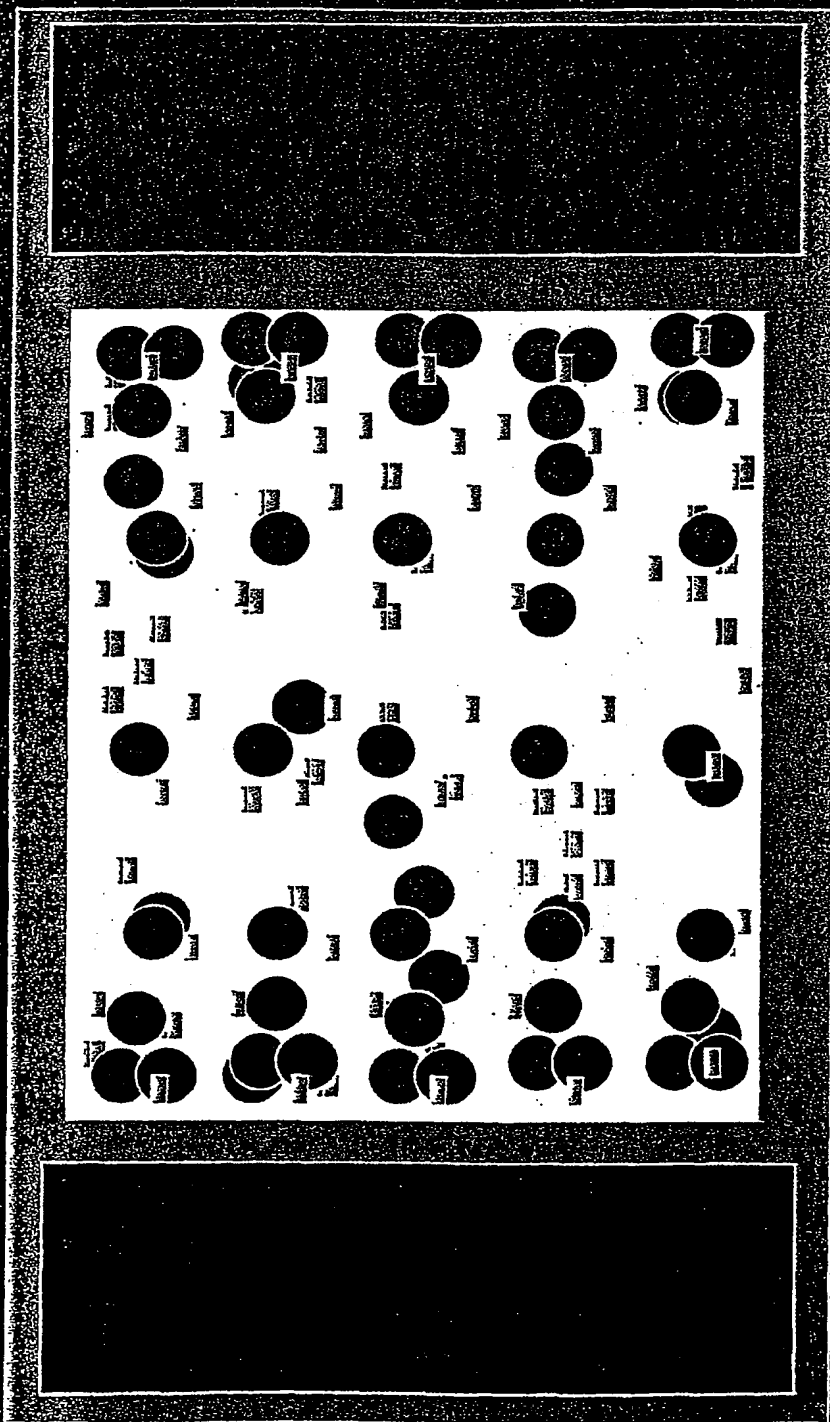
- Enzyme Discovery & Optimization
- Whole Cell Engineering
- Small Molecules
- Protein Therapeutics
- Antibodies
- Sequencing
- SNP's
- Proteomics
- RNA Dynamics
- Combi-Chem
- Compound Libraries

Consider GigaMatrix™ a 3D to 2D Converter

Fig. 43

CDIVERSA

Mixing With Paramagnetic Beads



- Reduced detection times
- Promote cell growth
- Uniformity

Fig 44

 DIVERSA

Mixing With Paramagnetic Beads

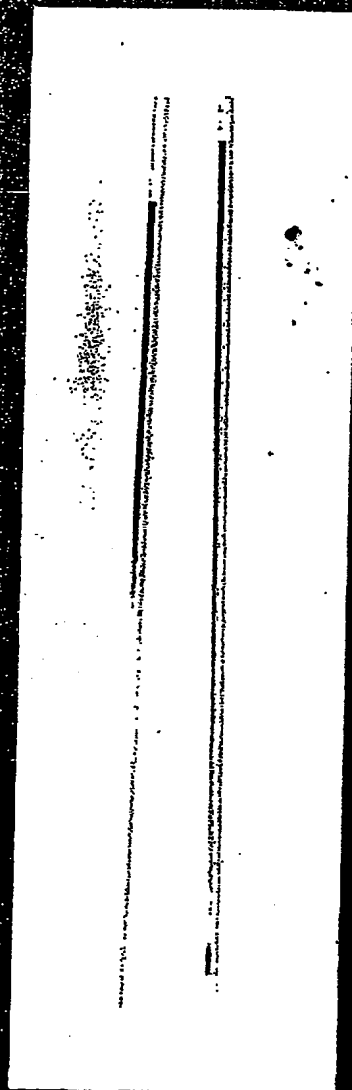
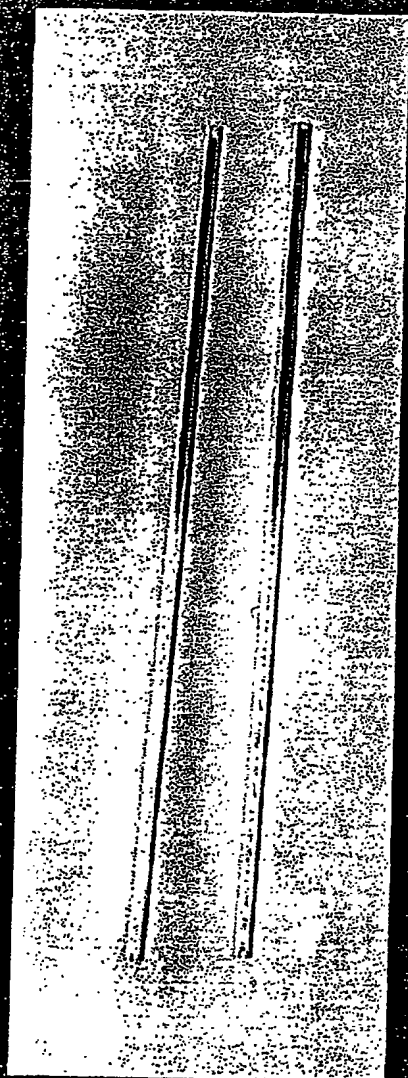


Fig. 45



DIVERSA

GigaMatrix™: Plate Density

Application	Well Diameter (μm)	Wells/ Plate	Volume* (nl)
Prototype	200	125,000	250
Nonlimiting Example: Mammalian	50	2,000,000	4
Nonlimiting Example: Bacterial	25	8,000,000	0.5
Nonlimiting Example: Process Limit	<5	128,000,000	0.007

* 40:1 length/diameter

Fig 46

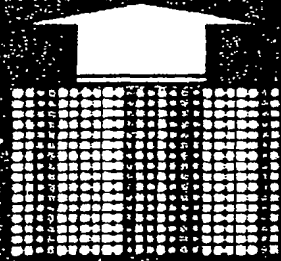
DIVERSA

Gene Site Saturation Mutagenesis™*

Dramatic improvements through small changes

GSSM™

Mutate ↓



UHTP Screen ↓

UHTP Screen is a high-throughput screening method for identifying and characterizing protein variants. It involves the use of a robotic platform to perform large-scale protein expression and screening. The process typically involves the following steps:

Combine Mutations ↓

Combine Mutations is a method for combining multiple mutations into a single protein variant. This is typically done using a combinatorial approach, where different mutations are introduced into a common DNA template and then screened for desired properties.

- Only comprehensive method (64 codons)
- Single, double, or triple codons
- Faster and more cost-effective
- Advantageous for protein therapeutics

*Issued US Patent Jan. 2001

30,000x Thermostability

Fig 47  DIVERSA

GeneReassembly™

Next generation evolution technology

Synthesis PCR Shuffling-

US Patent No. 5,965,408

Fragment Hybridization Method-

Patent Pending

GeneReassembly-

Patent Pending

• Most efficient gene family evolution methods

• Not restricted by relatedness of genes

• Enables screening efficiency

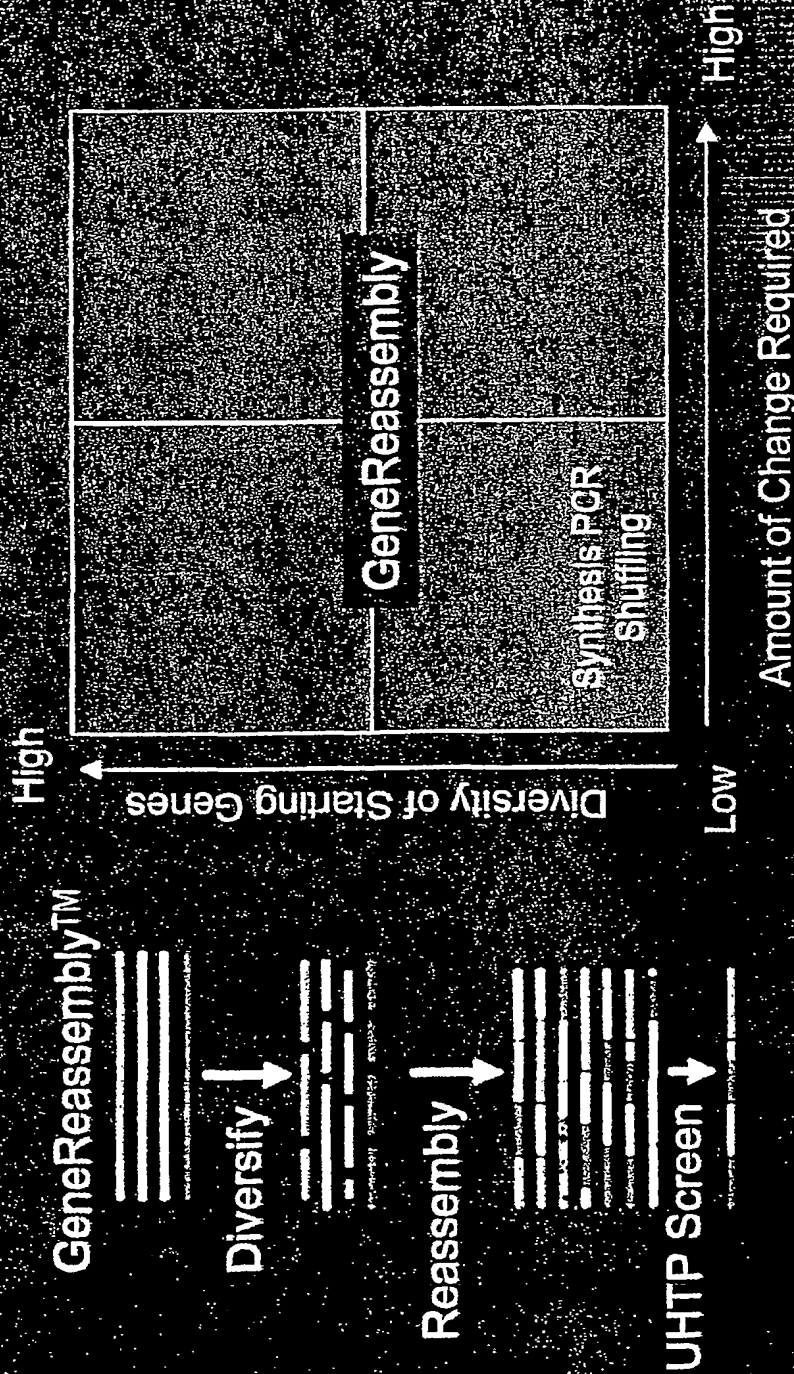
39,000x Activity

Fig 48

DIVERSA

GeneReassembly™

Best Method for Gene Product Improvement



39,000x Activity

Fig 49

GeneReassembly Experiment



828dI29
124dI48

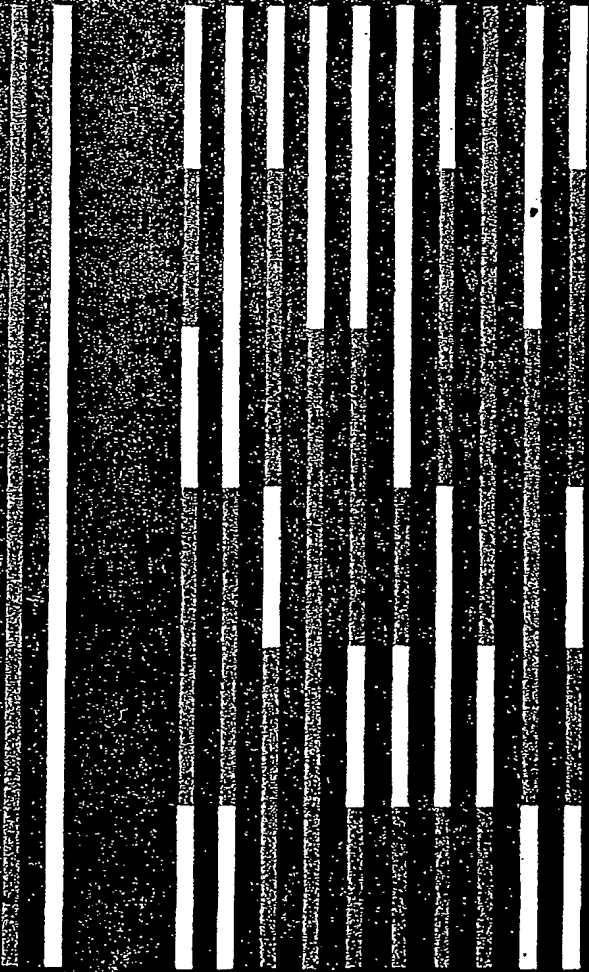


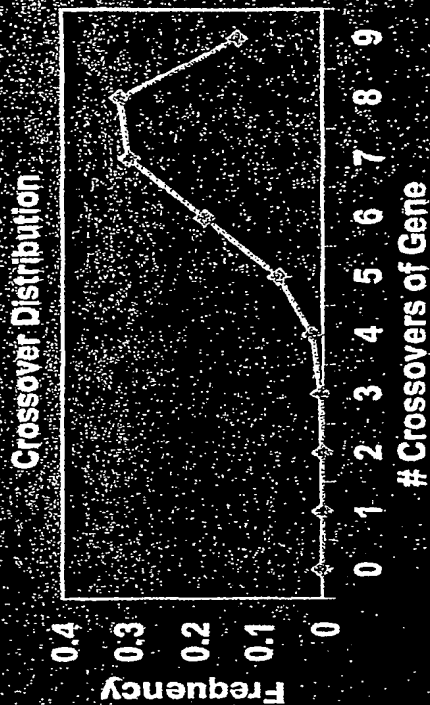
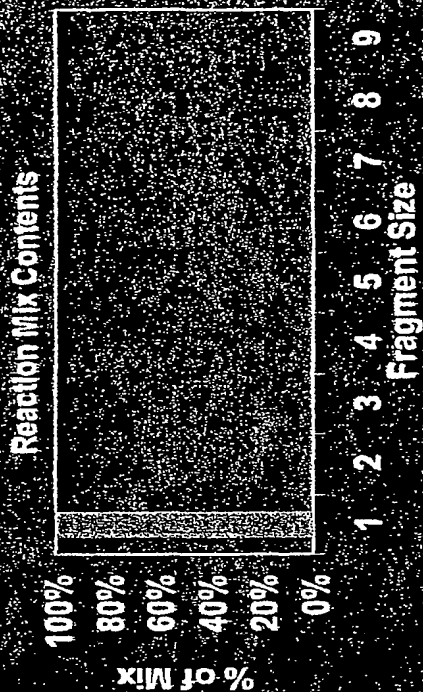
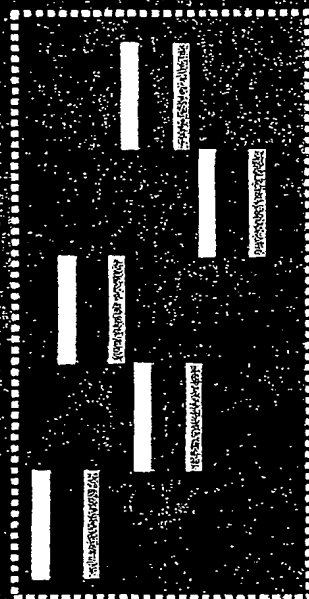
Fig 50



GeneReassembly™

Gene Family {  }

Reaction Mix



Typical
Reassembly
Products



Fig 51

Dehalogenase Reassembly

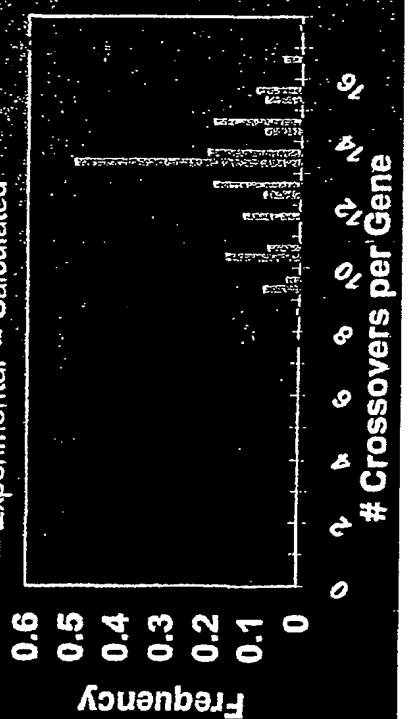


Myco
124-12
LinB
124-1d

Up
Mutants

Daughter
Clones

Crossover Distribution
Experimental Calculated



Crossover Location Distribution
Experimental Calculated

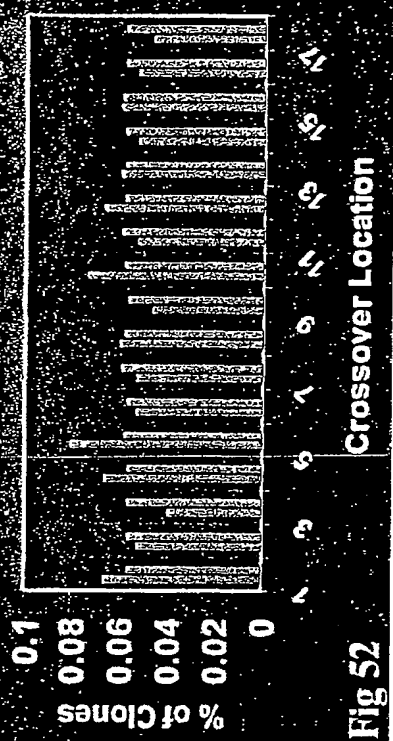
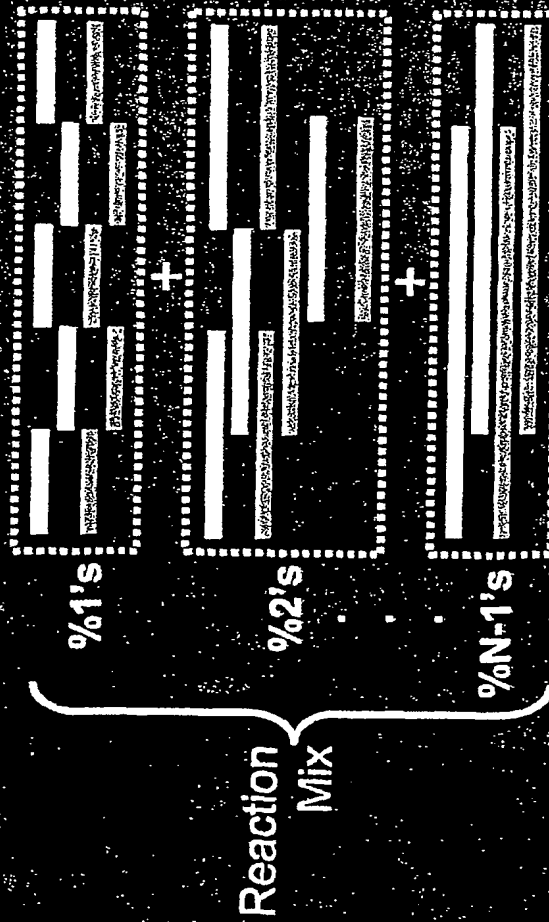


Fig 52

Tuneable-GeneReassembly™

Gene Family {



Typical Reassembly Products

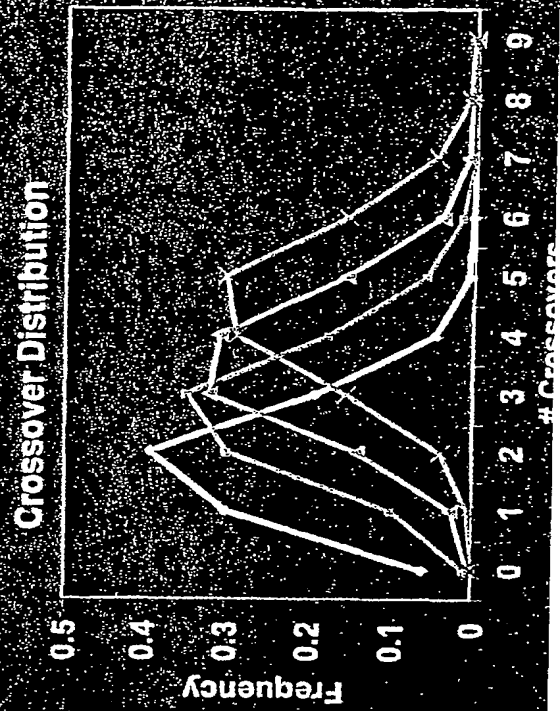
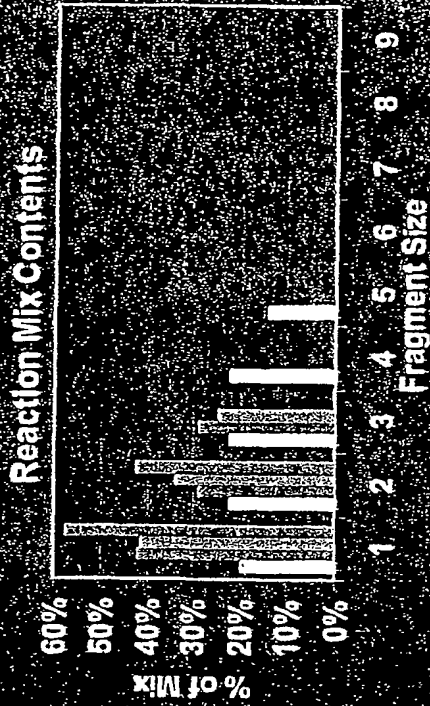


Fig 53

DNACarpenter™ – Reassembly Control Software

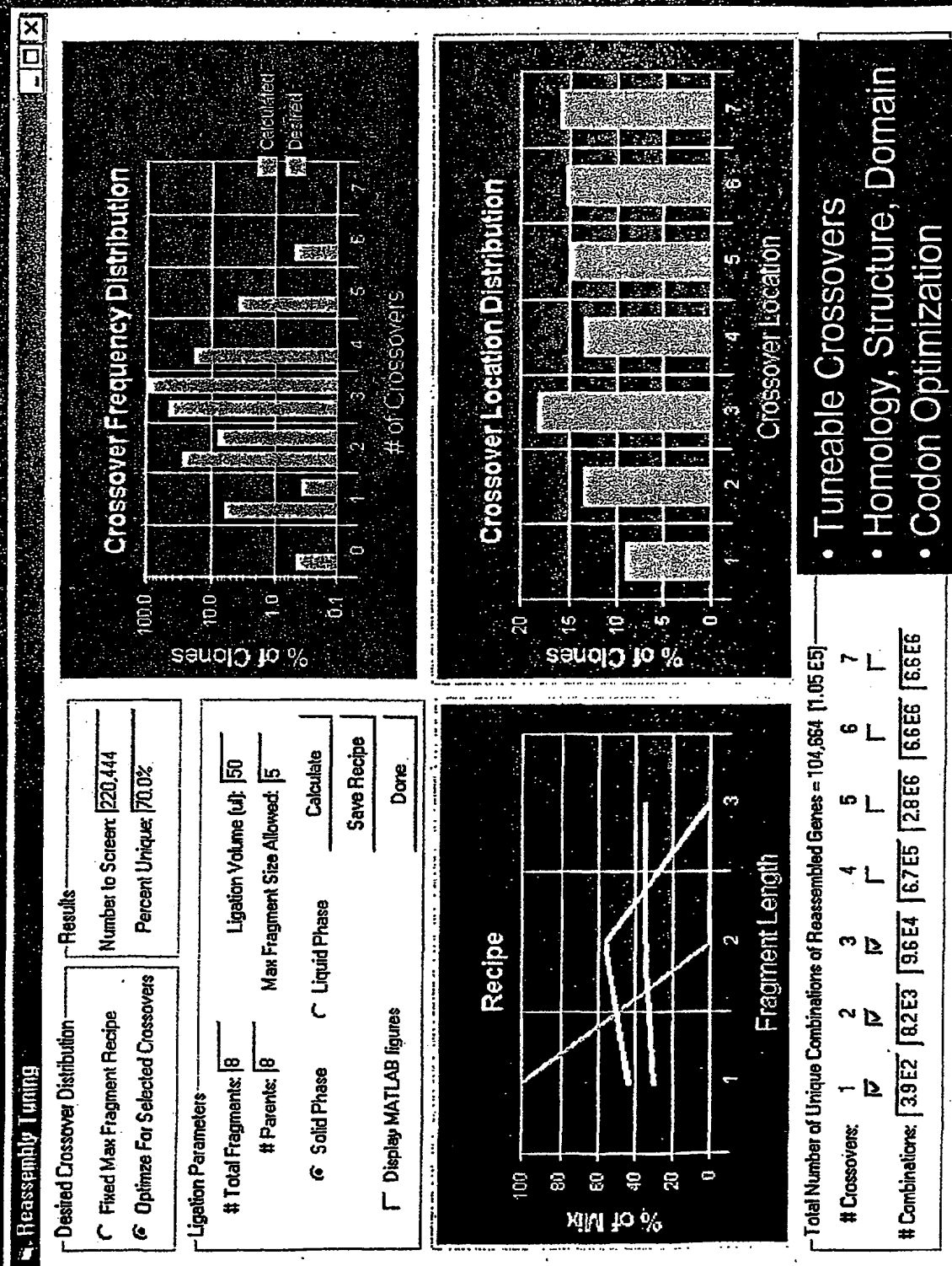


Fig 54

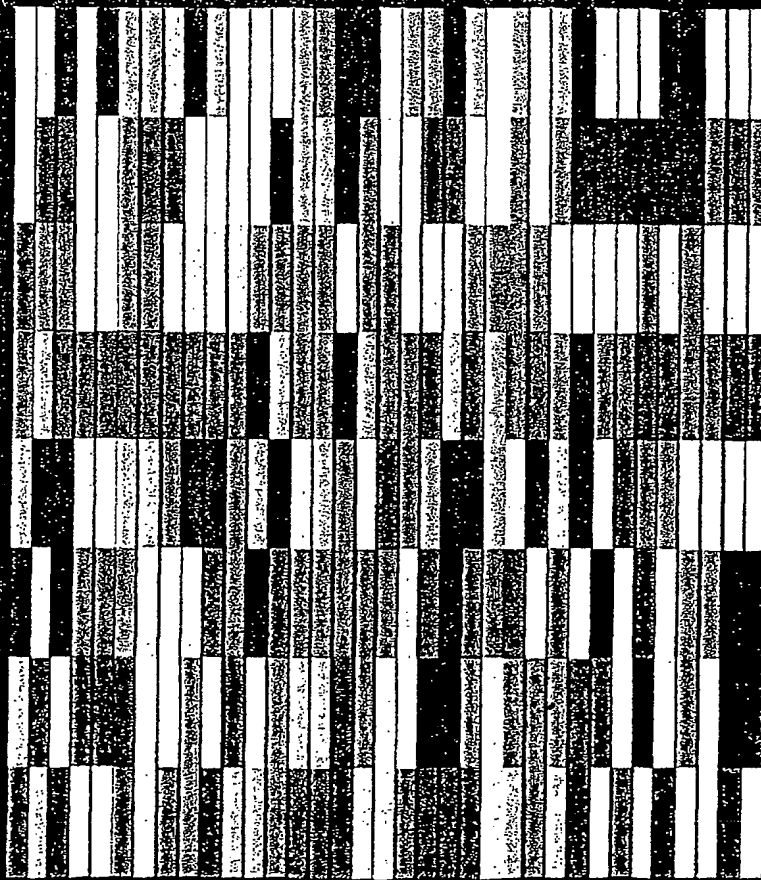
Plant Gene Family Reassembly Example



Parental
Genes



Up
Mutants



Crossover Distribution

Experimental Calculated



Crossover Location Distribution

Experimental Calculated

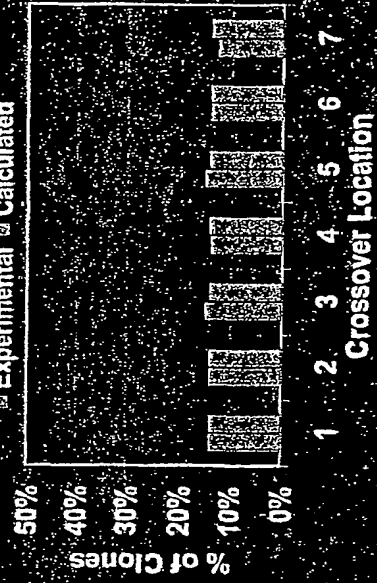


Fig 55



Fragment Pool

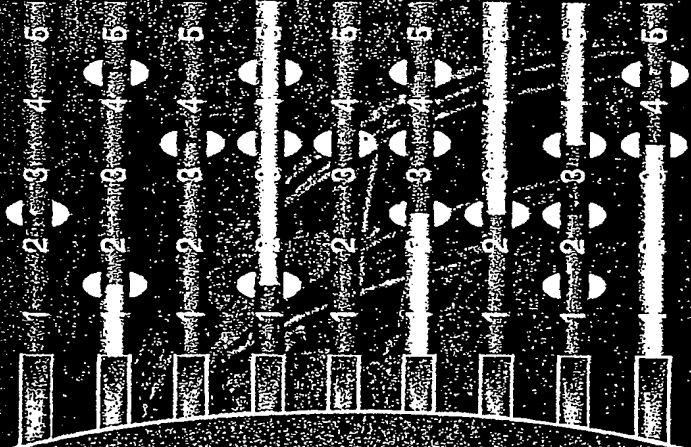
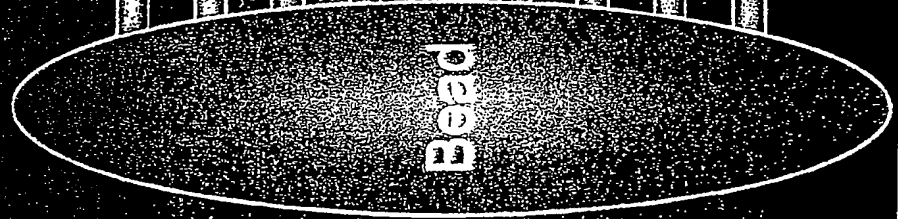
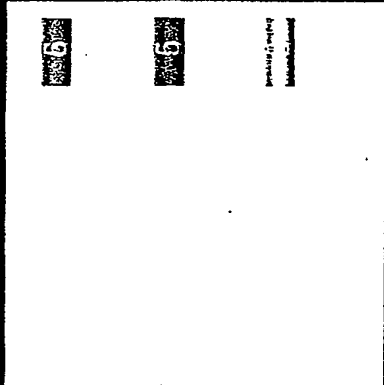


Fig 56

DIVERSA



Monoclonal Antibody Platform

Technologies

GeneReassembly™

GigaMatrix™

GSSM™

Fluorescent Proteins

Whole Cell Evolution

Capabilities

Human Antibody Generation

Increase Expression

Affinity Maturation

Improve Specificity

Parallel Screening



Fig 57  DIVERSA

Current Deficiencies in Antibody Generation

- Non-human or partially humanized antibodies
- Transgenic models hold incomplete human repertoire
- Slow process
- Suboptimal affinity and specificity
- Dependent upon phage or cell display
- Low manufacturing yields



Fig 58

DIVERSA



Diversa's Human Antibody System



Human Antibodies *without*-

Immunization

Transgenic Animals

Phage or Cell Display

Natubodies™

Antibody Characteristics-

100% Human Derived

High Affinity

High Throughput Generation

Optimized Expression

Fig 59

 DIVERSA

Antibody- Protein Structure

Bivalent Human Antibody

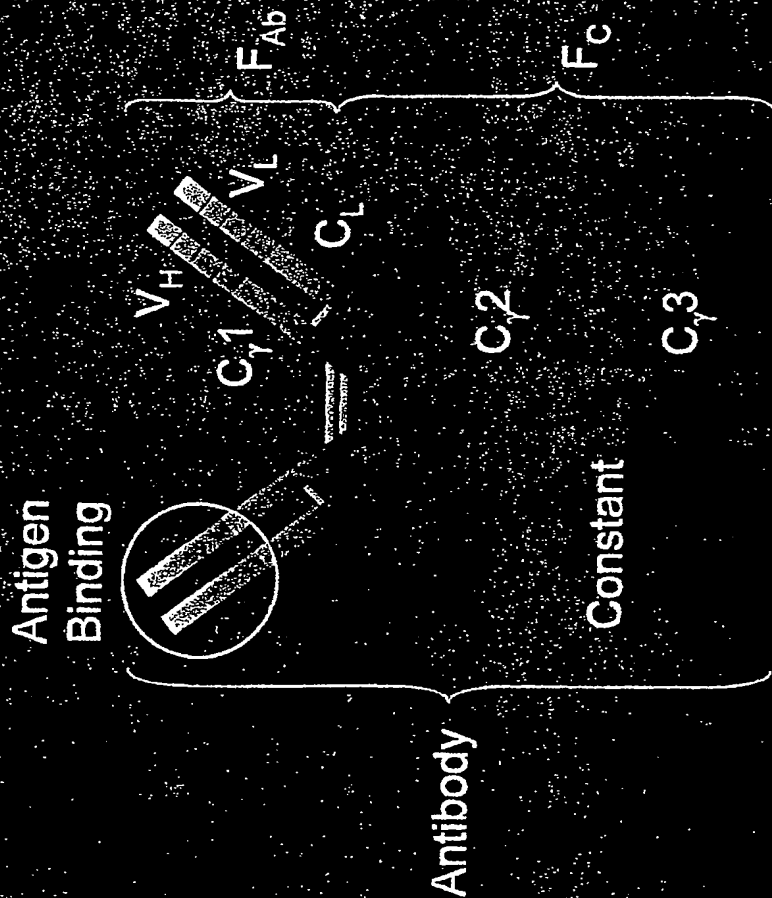


Fig 60

DRIVER

Pharmaceuticals – Human Antibodies

Synthetic Human Antibody Generation

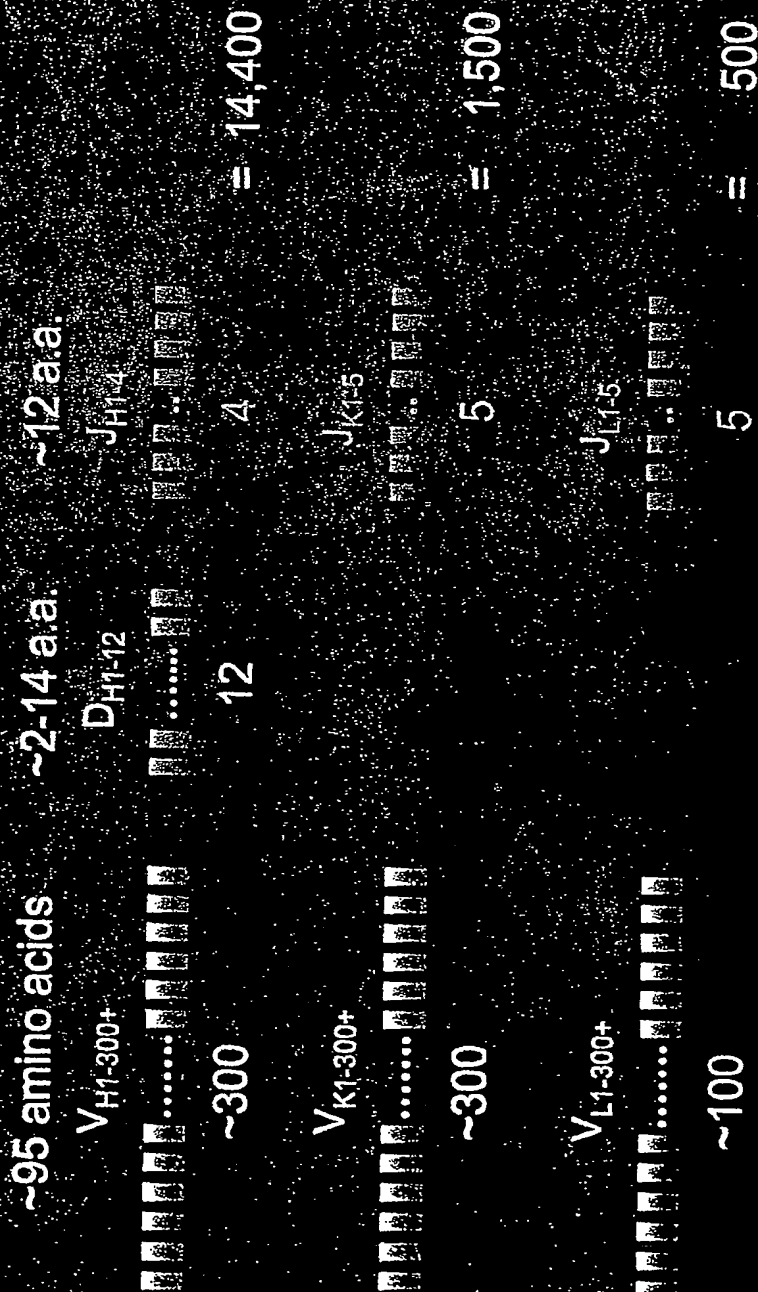
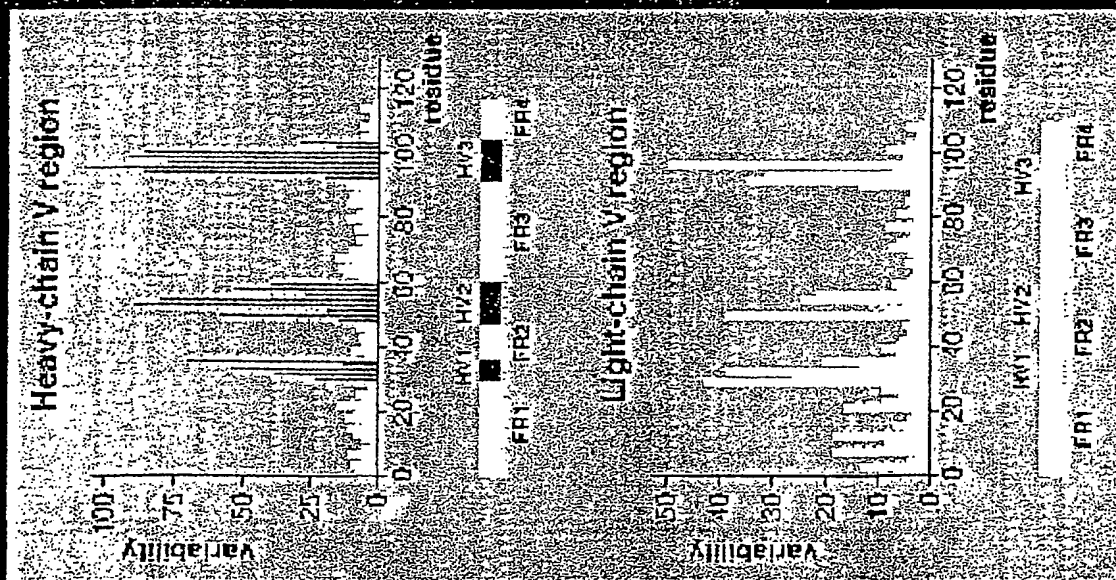


Fig 61 DIVERSA

Antibody V-Region Variability



$$\text{Variability} = \frac{\text{20 a.a.}}{\text{Freq. of most common a.a.}}$$

Fig 62  DIVERSA

Antibody Variable Region

Heavy-chain V region

CDR1 CDR2 CDR3



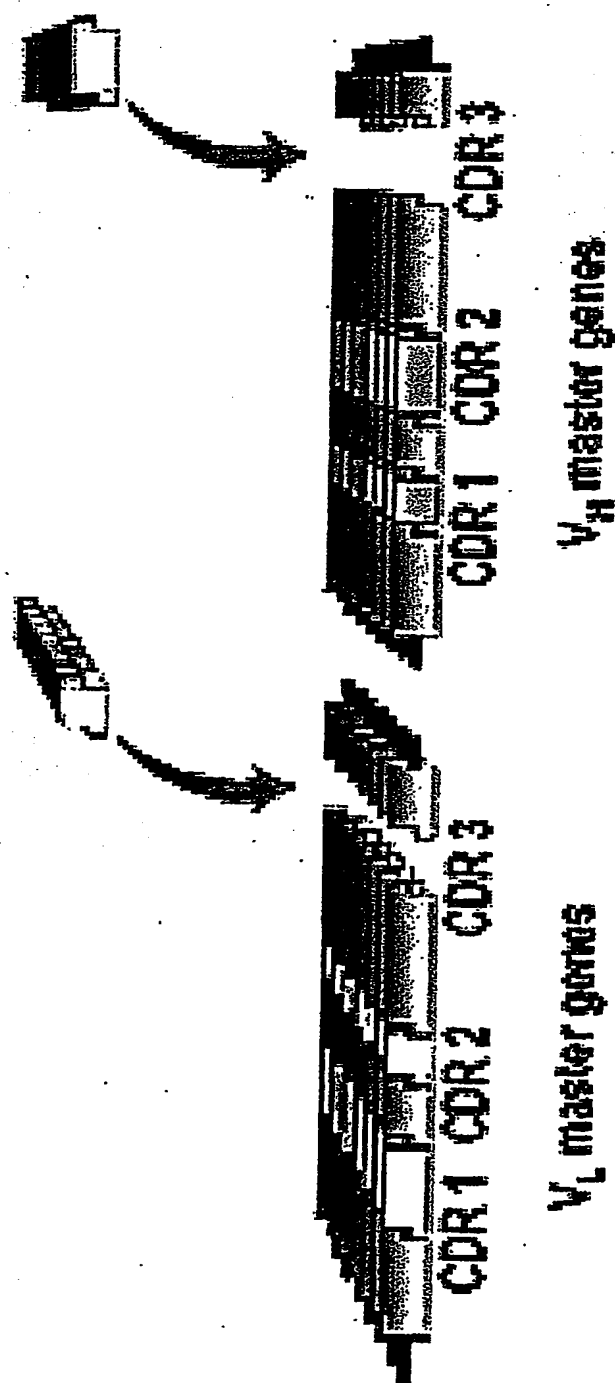
Light-chain V region (1 of 2)

CDR1 CDR2 CDR3



Heavy-chain V region = 900 \times 810,000
 Light-chain V region = 900 \times 270,000
 Light-chain V region = 300 \times >1 Million Reassembled CDR's*

*Additional permutations possible:
 from Framework region, D, J, species, artificial, etc.



Diversity: 49 human antibody frameworks covering structural diversity

Affinity: Completely modular gene structure by de novo synthesis

Fig 64

De novo Antibody Libraries



DIVERSA Approach

- GSSM
- Reassembly
- V_H / V_L genes with CDR 3
- FR2 & 3 Diversity

GigaMatrix

100% Human
Antibodies To All
Antigens



Fig 65

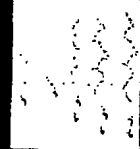
DIVERSA



Antibody Discovery



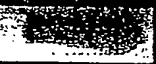
Human Ab Genes
Gene- Reassembly



Transform

Ab-GFP
Secreting Cells

Ag + His6



Mix

GigaMatrix™ Ab Screening



Loading
Plate

Grow

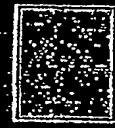


Compete



Ag

Mix ↓ Assay



Conc. w/
Magnet

Assay

Recover Clone ↓ Sequence

Note:

Antibody-GFP Fusion
Nickle-coated magnetic beads

Identify

Antibody Gene

Fig 66



GigaMatrix™ Antibody Discovery

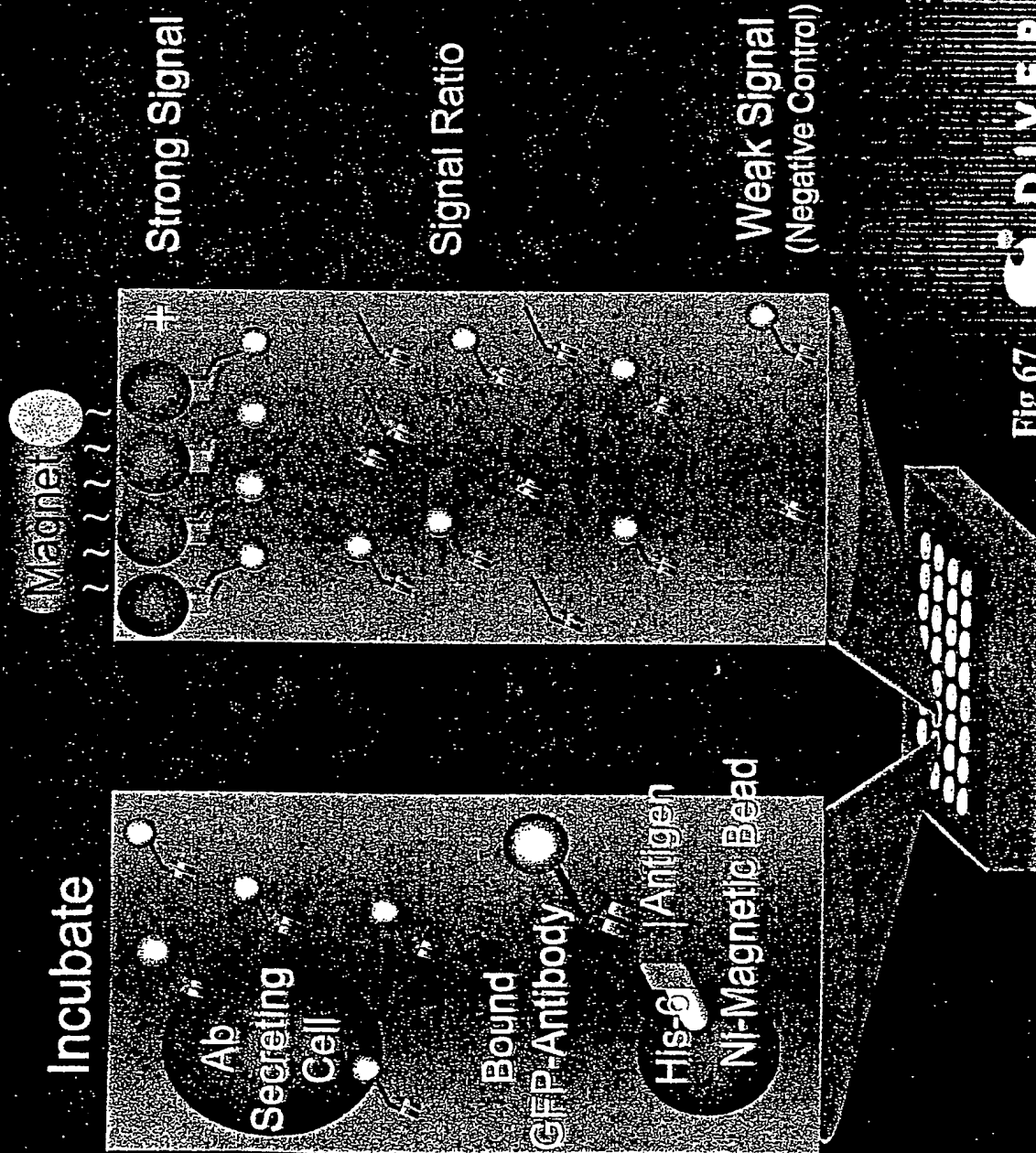


Fig 67 **DIVERSA**

Antibody Affinity Maturation

Multiplex GSSM, Gene Reassembly & HTP Screening

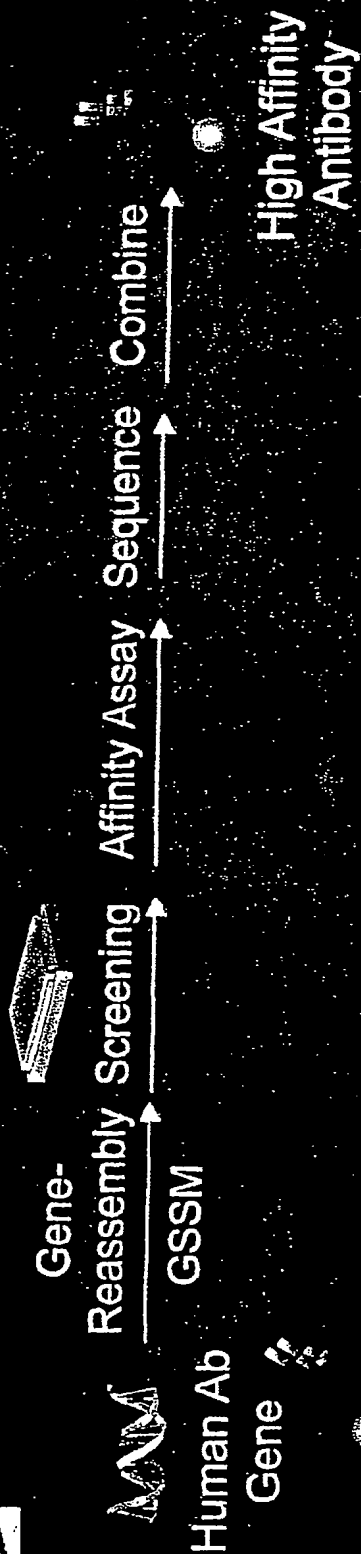


Fig 68



Multiple Rounds of GeneReassembly

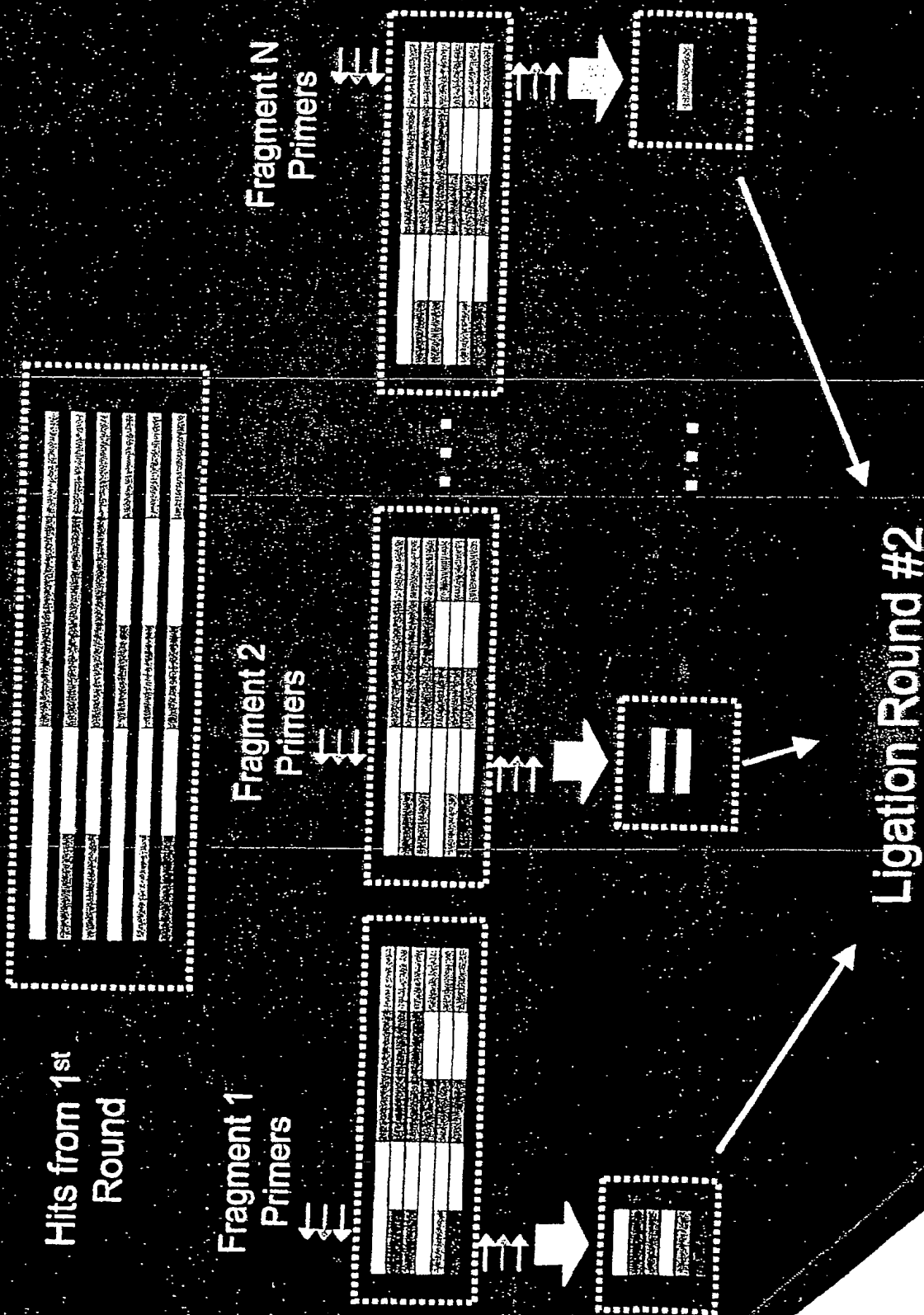


Fig 69